SPOURNCE LIGHTNO
SEQUENCE LISTING
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Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
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Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
40
Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser His
Glu Asp. Tyr. Ile Arg. Gln Phe. Leu Asn Ala. Gly. Lys. His. Val. Leu Val
Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Gln Glu Leu Trp Glu
100.
Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
115

	Leu Me	t. Glu	Glu	Phe Al	La. Phe.	Leu	Lys.	Lys.	Glu	Val.	Val.	Gly.	Lys.	Asp.			
	13	0			135.					140.							
,																	
	Leu Le	u Lys.	Gly.	Ser Le	eu Leu	Phe.	Thr.	Ser.	Asp.	Pro.	Leu	Glu	Glu	Asp.			
	145			15	50				155.					160			
	Arg. Pho	e Gly	Phe.	Pro. Al	La Phe	ser.	Gly.	Ile.	Ser	Arg.	Leu	Thr.	Trp.	Leu .			
		r. Leu	Phe	Glv Gl	lu Leu	Ser.	Leu '	Val.	Ser.	Ala.	Thr	Leu	Glu	Glu .			
<b>L</b>		s Glu	Asp	Gln Tv	ır Met	Lvs	Met. '	Thr	Val	Cvs	Leu	Glu	Th r	Glu			
		195	<u>-</u>			200					205						
		. 133.				200.					200.						
	Lus Lu	s Ser	Pro	T.e.ii Se	r Trn	Ťle	Glu	Gl 11	T.ve	G1 17	Pro	G1 v	T.e.11	T.VS			
<b>L</b>																	
Ul		0			215.					220.							
		2 7 2 4	Tur	Tou So	or Pho	ui c	Dho '	T 176	805	C1 11	cor	LOU	Cl.	7 cn			
<b>U</b>	223			4.	,				233.					240			
	Wal De	- 7	37-3	C1 17.	. 7 7	T	70	T1.	Db -	T	T	7	C1	7			
	Val. Pro	o Asn	var.	GIY. V	II. ASII.	ьуѕ.	Asn .	TTE.	Pne.	Leu	ьуѕ	ASP.	GIU	ASII.			
				245				250					255.				
<del></del>																	
†'	Ile. Pho	e Val.	GIn	Lys. Le	eu Leu	GT A	GIn :	Phe.	Ser	GLu	Lys.	GLu.	Leu	Ala.			
Ti.			260.				265					270.					
				_					_			_		_			
		. 275.				280.					285						
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	29	0			295.												
	*																
	<213>. 1	Homo.	sapie	ns													
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	atgaat	gcag. a	agccc	gagag.	gaagt	ttggc	gtg	gtgg	tgg.	ttgg	tgtt	gg. c	cgag	ccggc	120		
	tccgtg	egga t	tgagg	gactt.	gcggaa	atcca	. cac	cctt	cct.	cago	gttc	ct. g	aacc	tgatt	180	)	
	ggcttc	gtgt. (	cgaga	aggga.	gctcg	ggagc	att	gatg	gag.	tcca	gcag	at. t	tctt	tggag	240		
	gatgct	cttt. d	ccagc	caaga.	ggtgga	aggto	gcc1	tata	tct.	gcag	tgag	ag. c	tcca	gccat	300		
	gaggact	taca t	tcagg	cagtt.	ccttaa	atgct	. ggc	aagc	acg.	tcct	tgtg	ga. a	tacc	ccatg	360	)	
	acactg	tcat. t	tggcg	gccgc.	tcagga	aactg	, tgg	gagc	tgg.	ctga	gcag	aa a	ggaa	aagtc	420	)	
						2.											

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	ttgcacgagg. agcatgttga. actcttgatg. gaggaattcg. ctttcctgaa. aaaagaagtg. 480	
:	gtggggaaag, acctgctgaa, agggtcgctc, ctcttcacat, ctgacccgtt, ggaagaagac, 540,	
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	gtgccaaatg taggagtgaa taagaacata tttctgaaag atcaaaatat atttgtccag 840	
	aaactettgg. gecagttete. tgagaaggaa. etggetgetg. aaaagaaaeg. eateetgeae. 900	
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	<pre>&lt;213&gt; Homo sapiens</pre>	
U	<400> 3	
	Met. Asn Thr. Glu Pro. Glu Arg. Lys. Phe. Gly. Val. Val. Val. Gly. Val	
<b>U</b> I	1	
	Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro	
	20	
<b>L</b>		
. Fi	Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu	
	Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser	
	50 55 60 60	
	•	
	Ser Gln Glu Val. Glu Val. Ala Tyr Ile Cys Ser Glu Ser Ser Ser His	
	65	
	Glu Asp. Tyr. Ile Arg. Gln Phe. Leu Asn. Ala. Gly. Lys. His. Val. Leu Val	
	Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu	
	100.	
	Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu	
	115	
	Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp	
	130	
	:	
	Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu Glu	
	145	

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Arg. Phe. Gly. Phe. Pro. Ala Phe. Ser. Gly. Ile. Ser. Arg. Leu Thr. Trp. Leu
180
Arg. Lys. Glu Asp. Gln Tyr. Met. Lys. Met. Thr. Val. Cys. Leu Glu Thr. Glu
Lys. Lys. Ser. Pro. Leu Ser. Trp. Ile. Glu Glu Lys. Gly. Pro. Gly. Leu Lys.
210
Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
225 240
235
Val. Pro Asn Val. Gly Val. Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
[f]
Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
<b>√</b> 260 265 270
Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
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F
Gln Lys Tyr Cys Cys Ser Arg Lys
Ti
295
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290 295  <210> 4  <211> 295  <211> PRT
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65	70	75	
	Arg Gln Phe Leu	Gln Ala Gly Lys His V	Val. Leu Val. Glu
	<del>-</del>		95
	Thr Leu Ser Phe	Ala Ala Ala Gln Glu I	Leu Trp. Glu Leu
			110
	. 100	100.	110
	Tue Clu Ara Val	Leu Wie Clu Clu Wie V	Val. Glu Leu Leu
		120	L <b>2</b> 5
wat ole ole	Dhe Clu Dhe Ieu	Des Des Classical Cons	The Toron Charles
			Gly Lys Glu Leu
	135.		
	,		
			Glu Glu Arg
	150	155	
Phe. Gly. Phe.	. Pro. Ala. Phe. Ser.	Gly Ile Ser Arg Leu T	Chr. Trp. Leu Val
	165	170	Thr. Trp. Leu Val.
Tilling Ser Leu Phe			Leu Glu Glu Arg
<u></u>	180	185	190
Lys Glu Asp.	. Gln Tyr. Met. Lys.	Met. Thr. Val. Gln Leu G	Glu Thr Gln Asn
<u></u>		200	205
	•		
Lys. Gly. Leu	Leu Ser Trp Ile	Glu Glu Lys. Gly. Pro. G	Sly Leu Lys Arg
210	215.		
Asn Arg Tyr.	Val Asn Phe Gln	Phe Thr. Ser. Gly. Ser. I	Leu Glu Glu Val
225	230	235	240
Pro Ser Val.	Gly Val. Asn Lys.	Asn Ile. Phe. Leu Lys. A	Asp. Gln Asp. Ile
			255
	Lys. Leu Leu Asp.	Gln Val. Ser. Ala. Glu A	Asp. Leu Ala Ala
			270
	Arg Ile Met His	Cvs Leu Gly Leu Ala S	Ser. Asp. Ile. Gln
	=	<del>-</del>	285
	His Gln Lue Lue		
		E	
		J	

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gaaatttgga gtggtagtgg ttggtgttgg cagagctggc tcggtgaggc tgagggactt 180
gaaggatcca cgctctgcag cattcctgaa cctgattgga tttgtgtcca gacgagagct 240
tgggagcctt gatgaagtac ggcagatttc tttggaagat gctctccgaa gccaagagat 300
tgatgtcgcc tatatttgca gtgagagttc cagccatgaa gactatatac ggcagtttct 360
gcaggctggc aagcatgtcc tcgtggaata ccccatgaca ctgtcatttg cggcggccca 420
ggagctgtgg. gagctggccg. cacagaaagg. gagagtcctg. catgaggagc. acgtggaact. 480
cttgatggag. gaattcgaat. tcctgagaag. agaagtgttg. gggaaagagc. tactgaaagg. 540
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fig tgtaaacttc cagttcactt ctgggtccct ggaggaagtg ccaagtgtag gggtcaataa 840
gaacattttc ctgaaagatc aggatatatt tgttcagaag ctcttagacc aggtctctgc 900
: "alling and agaggaccig goigoigaga agaagogoal caigcaligo cigggoligg coagogacal 960
ccagaagett. tgccaccaga agaagtgaag aggaagette agagaettet gaaggggee 1020
agggtttggt. cctatcaacc. attcaccttt. agctcttaca. attaaacatg. tcagataaac. 1080
a1081
<213> Artificial Sequence
<pre>&lt;223&gt; Description of Artificial Sequence: hydrophobic</pre>
domain of BVR
domain of byk
<221> PEPTIDE
<222> (2)
<pre></pre> <pre>&lt;222&gt; Where X is any aa</pre>
Phe. Xaa Val. Val. Val
· · · · · · · · · <211> 6 · · · · · · · · · · · · · · · · · ·
<212> PRT.:
<213> Artificial Sequence
-

(0.00)
<220>
<pre>&lt;223&gt; Description of Artificial Sequence: nucleotide</pre>
binding domain of BVR
<222>. (2)
<220>
<221> PEPTIDE
E a gamin
Gly Xaa Gly Xaa Xaa Gly
₹155
[ <210>. 8
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oxidoreductase domain of BVR
<210> 9
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zipper of BVR
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<221> PEPTIDE
·
<220>
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Leu Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Lys Xaa
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Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Leu
20
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<220>
of. BVR
<400>. 10
Ser Arg Arg
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<211>. 3
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of BVR
• • • • • • • •
· · · · · · · · <400> 11 · · · · · · · · · · · · · · · · · ·
Lys Gly Ser

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	of BVR
	<220>
	<221> PEPTIDE
. <u>L.s.</u>	<222>. (3)
3	<pre>&lt;223&gt; where X is any aa</pre>
king.	
	<pre>&lt;400&gt; 12</pre>
1 Fi	plan mlani yana
. <del>.</del>	Phe. Thr. Xaa.
	l
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₽   	
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Mi	<220>
· =·	<pre>&lt;223&gt; Description of Artificial Sequence: nuclear</pre>
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<u> </u>	
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了: [f]	His. Cys. Xaa. Xaa. Xaa. Xaa. Xaa. Xaa. Xaa. Xa
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# · · · · · · · · · · · · · · · · · · ·	<210> 16
	<211> 7
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[-1	<213> Artificial Sequence
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	<223> Description of Artificial Sequence: protein
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	:

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	<221> PEPTIDE
	<222> (5)(7)
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	Gln Lys Xaa Cys Xaa Xaa Xaa Lys
	1
<b>.</b>	
·	$\cdot$
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<b>5</b>	
<b></b> .	
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